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1204

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/848,798

DATE: 12/26/2001

TIME: 15:52:19

Input Set : N:\Crif3\RULE60\09848798.raw

Output Set: N:\CRF3\12262001\I848798.raw

1 <110> APPLICANT: Siegel, Donald L.
2 <120> TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
3 SORTING METHOD FOR PRODUCTION THEREOF
4 <130> FILE REFERENCE: 09596-42U2
5 <140> CURRENT APPLICATION NUMBER: 09/848,798
6 <141> CURRENT FILING DATE: 2001-05-04
7 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
12 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
W--> 13 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
14 <160> NUMBER OF SEQ ID NOS: 224
15 <170> SOFTWARE: PatentIn Ver. 2.0
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18 <211> LENGTH: 128
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
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26 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
27 20 25 30
28 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
29 35 40 45
30 Ala Ala Thr Ala Tyr Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
31 50 55 60
32 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
33 65 70 75 80
34 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Phe Tyr Cys
35 85 90 95
36 Ala Arg Gly Gly Phe Tyr Tyr Asp Ser Ser Gly Tyr Tyr Gly Leu Arg
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46 <223> OTHER INFORMATION: anti-Rh(D) chain C01
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49 1 5 10 15
50 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
51 20 25 30
52 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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53          35          40          45
54  Ser Val Ile Ser Tyr Asp Gly His His Lys Asn Tyr Ala Asp Ser Val
55          50          55          60
56  Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr
57          65          70          75          80
58  Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
59          85          90          95
60  Ala Asn Leu Arg Gly Glu Val Thr Arg Arg Ala Ser Val Pro Phe Asp
61          100          105          110
62  Ile Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser
63          115          120
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74  Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
75      20          25          30
76  Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
77      35          40          45
78  Ser Val Ile Ser Tyr Asp Gly His His Lys Asn Tyr Ala Asp Ser Val
79      50          55          60
80  Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr
81      65          70          75          80
82  Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
83          85          90          95
84  Ala Asn Leu Arg Gly Glu Val Thr Arg Arg Ala Ser Val Pro Phe Asp
85          100          105          110
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87          115          120
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91 <212> TYPE: PRT
92 <213> ORGANISM: Homo sapiens
93 <220> FEATURE:
94 <223> OTHER INFORMATION: anti-Rh(D) chain C04
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97      1          5          10          15
98  Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Thr Tyr
99      20          25          30
100  Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
101      35          40          45
102  Ser Val Ile Ser Tyr Asp Gly His Asn Lys Asn Tyr Ala Asp Ser Val
103      50          55          60

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104      Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr
105          65              70              75              80
106      Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
107              85              90              95
108      Ala Asn Leu Arg Gly Glu Val Thr Arg Arg Ala Ser Ile Pro Phe Asp
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111              115              120
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115 <212> TYPE: PRT
116 <213> ORGANISM: Homo sapiens
117 <220> FEATURE:
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119 <400> SEQUENCE: 5
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121          1              5              10              15
122      Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
123              20              25              30
124      Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
125              35              40              45
126      Ala Val Ile Ser Tyr Asp Gly Thr Asn Lys Tyr Phe Ala Asp Ser Val
127          50              55              60
128      Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr
129          65              70              75              80
130      Leu Gln Met Thr Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Phe Cys
131              85              90              95
132      Ala Asn Leu Arg Gly Glu Val Thr Arg Arg Ala Ser Val Pro Leu Asp
133              100              105              110
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135              115              120
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139 <212> TYPE: PRT
140 <213> ORGANISM: Homo sapiens
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145          1              5              10              15
146      Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
147              20              25              30
148      Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
149              35              40              45
150      Ala Val Ile Ser Tyr Asp Gly Thr Asn Lys Tyr Phe Ala Asp Ser Val
151          50              55              60
152      Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr
153          65              70              75              80
154      Leu Gln Met Thr Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Phe Cys

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155                      85                      90                      95
156      Ala Asn Leu Arg Gly Glu Val Thr Arg Arg Ala Ser Val Pro Leu Asp
157                      100                      105                      110
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159                      115                      120
161 <210> SEQ ID NO: 7
162 <211> LENGTH: 124
163 <212> TYPE: PRT
164 <213> ORGANISM: Homo sapiens
165 <220> FEATURE:
166 <223> OTHER INFORMATION: anti-Rh(D) chain C10
167 <400> SEQUENCE: 7
168      Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
169      1                      5                      10                      15
170      Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
171                      20                      25                      30
172      Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
173                      35                      40                      45
174      Ser Val Ile Ser Tyr Asp Gly His His Lys Asn Tyr Ala Asp Ser Val
175                      50                      55                      60
176      Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Lys Thr Leu Tyr
177      65                      70                      75                      80
178      Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
179                      85                      90                      95
180      Ala Asn Leu Arg Gly Glu Val Thr Arg Arg Ala Ser Val Pro Phe Asp
181                      100                      105                      110
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186 <211> LENGTH: 125
187 <212> TYPE: PRT
188 <213> ORGANISM: Homo sapiens
189 <220> FEATURE:
190 <223> OTHER INFORMATION: anti-Rh(D) chain D01
191 <400> SEQUENCE: 8
192      Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
193      1                      5                      10                      15
194      Ser Leu Arg Leu Ser Cys Val Val Ser Gly Phe Thr Phe Asn Asn Tyr
195                      20                      25                      30
196      Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
197                      35                      40                      45
198      Ala Val Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
199                      50                      55                      60
200      Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
201      65                      70                      75                      80
202      Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
203                      85                      90                      95
204      Ala Arg Glu Asn Gln Ile Lys Leu Trp Ser Arg Tyr Leu Tyr Tyr Phe
205                      100                      105                      110

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213 <220> FEATURE:
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215 <400> SEQUENCE: 9
216      Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
217              1                      5                      10                      15
218      Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
219              20                      25                      30
220      Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
221              35                      40                      45
222      Ala Val Ile Trp Phe Asp Gly Ser Asn Lys Glu Tyr Ala Asp Ser Val
223              50                      55                      60
224      Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
225              65                      70                      75                      80
226      Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
227              85                      90                      95
228      Ala Arg Glu Glu Val Val Arg Gly Val Ile Leu Trp Ser Arg Lys Phe
229              100                      105                      110
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231              115                      120                      125
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235 <212> TYPE: PRT
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240      Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Ala Gln Pro Gly Arg
241              1                      5                      10                      15
242      Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Ser Leu Arg Ser Tyr
243              20                      25                      30
244      Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
245              35                      40                      45
246      Ala Asp Ile Trp Phe Asp Gly Ser Asn Lys Asp Tyr Ala Asp Ser Val
247              50                      55                      60
248      Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
249              65                      70                      75                      80
250      Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
251              85                      90                      95
252      Ala Arg Asp Trp Arg Val Arg Ala Phe Ser Ser Gly Trp Leu Ser Ala
253              100                      105                      110
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255              115                      120                      125
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/848,798

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